

378/550

FIGURE 378

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIMLFRPHTMPKYLLGSVNKS
VVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQKIQVTVDDPVTKPVVQIHPPSGAVEY
VGNMTLTCHVEGGTRLAYQWLKNGREPVHTSSTYSFSPQNNTLHIAVPVKEDIGNYSCLVRNPFVSEMESDIIMPII
YYGPGYGLQVNSDKGLKVGVEFTVOLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMD
YVCAYNNITGRQDETHFTVIITSVGLKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQKLEG
RPETEYRKAQTFSGHEDALDDFGIYEFVAFEDVSGVSRIPSRVSPASDCVSGQDLHSTVYEVIIQHIIPAQQQDHPE

Important features:**Signal sequence:**

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208, 276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237, 239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

379/550

FIGURE 379

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTACATGGGCACAA
TTTCACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTGT
CTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCAAGC
GCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCTTTAA
TTAAGGGGTTACATCCAACCCAGAGCGCTTTTGPGGGCACTGATTGCTCCAGCTTCTGCGTC
ACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGACATGTATAGACACAAAAACAGCTG
GAGATTGGGCTTAAAATACCCACCAAGCTCCAAGAAGAGACCCAAGTCCCCAAACATTGAT
TTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCAGCCCACAA
GATGCCATTGTCCCCGGCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCT
GCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCAGCATATGCAGGAAGCGGCAGGAATAAG
GAAAAGCAGCCTCCTGACTTTCTCGCTTGSTGGTTTGAGTGGACCTCCAGGCCAGTGCCGG
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCA
ATCGCGCGCCGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAA
ATAG

380/550

FIGURE 380

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLLS
GATATAALPLEGGPTGRDSEHMQEAAAGIRKSLLTFLAWWFEWTSQASAGPLIGEEAREVARR
QEGAPPQQSARRDRMPCRNFFWKTFSSCK

Important features:

Transmembrane domain:

amino acids 51-69

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 35-39, 92-96

N-myristoylation sites.

amino acids 64-70, 75-81, 90-96

Amidation site.

amino acids 33-37

381/550

FIGURE 381

GGCGCCGGTGACACGGGGCGGGCTGAGCGCCTCCTGCGGGCCGGGCTGCGCGCCCCGGGCCCGCC
GGCGCGCCACGCCCCAACCCCCGGCCGCGCCCCCTAGCCCCCGCCCGGGGCCCGCGCCCGCGCC
CCGCGCCCAAGGTGAGCGCTCCGCCCCGCGCGAGGCCCGCCCGGCCCGCCCGCCCGCCCGCC
CGCGCGCGGGGGAACCGGGCGGATTCTCGCGCTCAAACCACCTGATCCCATAAACATTTC
ATCCTCCCGGGCGCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCGCCGCGCCGCCCTCGCCCTG
TGCGCCTGCGCGCCCTGCGCACCCGCGGCCGAGCCAGCCAGACCGGGCGGAGCGGAGCG
CGCCGAGCCTCGTCCCGCGGCCGGGCCGGGGCCGGGCCGTAGCGGGCGCGCCTGGATGCGGAC
CCGGCCGCGGGGAGACGGGCGCCCGCCCGAAACGACTTTCAGTCCCCGACGCGCCCGCCCCA
ACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTGCTGTGGCTG
CAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCGTATGCTACAATGAGCCCAAGGTG
ACGACAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCGTGGGCATCCCTGCTGCCAGCCAG
CGCATCTTCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTCCGTGCTGCCG
AACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGCGGCTGCCCTTCACT
GGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCCGGTCTGTGGACCCCT
GCCACATTCACGGCCTGGGGCCGCTACACACGCTGCACCTGGACCGCTGCGGCCTGCAGGAG
CTGGGCCCGGGCTGTTCCGCGGCTGGCTGCCCTGCAGTACCTCTACCTGCAGGACAACGCG
CTGCAGGCACTGCCGTGATGACACCTTCCGCGACCTGGGCAACCTCACACACCTCTTCTGCAC
GGCAACCGCATCTCCAGCGTGCCGAGCGCGCCTTCCGTGGGCTGCACAGCCTCGACCGTCTC
TACTGCACAGAACCGCGCTGGCCCATGTGCACCCGCAATGCTTCCGTGACCTTGGCCGCTC
ATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCACTGAGGCGCTGGCCCCCTG
CGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTGTGTGACTGCGGGGACGCCCA
CTCTGGGCCCTGGCTGCAAGAAGTTCGCGGGCTCCTCCTCCGAGGTGCCCTGCAGCCTCCCGCAA
CGCCTGGCTGGCCGTGACCTCAAACGCTAGCTGCCAATGACCTGCAGGGCTGCGCTGTGGCC
ACCGGCCCTTACCATCCCATCTGGACCGGACGGCCACCGATGAGGACCGCTGGGGCTTCCC
AAGTGCTGCCAGCCAGATGCCGCTGACAAGGCTCAGTACTGGAGCTGGAAGACCAGCTTCG
GCAGGCAATGCGCTGAAGGGACCGCTGCCGCCCGGTGACAGCCCGCCGGGCAACGGCTCTGGC
CCACGGCACATCAATGACTCACCTTTGGGACTCTGCCTGGCTCTGCTGAGCCCCGCTCACT
GCAGTGGGGCCGAGGGCTCCGAGGCCACAGGGTTCCCCACCTCGGGCCCTCGCCGGAGGCCA
GGCTGTTTACGCAAGAACCGCACCCGAGCCACTGCCGTCTGGGCCAGGCGAGCGGGGGT
GGCGGACTGGTGACTCAGAAGGCTCAGGTGCCCTACCCAGCCTACCTGCAGCCTCACCCCC
CTGGGCTGCGCTGGTGTGTGGACAGTGCTTGGGCCCTGCTGAACCCCCAGCGGACACAAGA
GCGTGCTCAGCAGCCAGGTGTGTGTATACATACGGGGTCTCTCTCCACGCCCAAGCCAGCCGG
GCGGCCACCCGTGGGGCAGGCCAGGCCAGGTCTCCCTGATGGACGCGCTGCCGCCGCCACC
CCCATCTCCACCCCATCATGTGTTACAGGGTTCGGCGGCGAGCGTTTGTTCAGAACCGCCCTC
CCACCCAGATGCGCGTATATAGAGATATGCATTTTATTTTACTGTGTAATAATATCGGACGA
CGTGAATAAAGAGCTCTTTTCTTAAAAAA

382/550

FIGURE 382

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRIF
LHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAAF TGLALLEQLDLSDNAQLRSVDPATF
HGLGRLHTLHLDRCGLQELGPG LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLHGNR
ISSVPERAFRGLHSLDRLLHQN RVAVHVP HAFRDLGR LMTLYLFANNLSALPTEALAPLRAL
QYLR LNDNPWVCD CRARPLWANLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGC AVATGP
YHPIW TGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGNGSGPRH
INDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQAGSGGGGT
GDSEGGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

383/550

FIGURE 383

TTCGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCCTCTAAGAAGGGGGAGTCCTGAACCTGTCTCG
AAGCCCTTGTCCGTAAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCGAGGGACCTTTCCTGCTCTTTGTAGGG
ACTTCTTTCTCTGCTTCAGCAACATGAGGCTTTCTTGTGGAACGCGGTCCTGACCTGCTTCGTCACTTCTTTGA
TTGGGGCTTTGATCCCTGAACCGAGAAGTGAAAATGAAGTTCCGAGAAGCCATTCATCTGCCATTCGCAAGACCA
AAGGAGGGGATTGTGATTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTCACA
AACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGTTGGGACCGAGGCTTGA
AAGGAATGTGTAGGAGAGAGAAGAAAGCTCATCATTTCTCTGCTCTGGGCTATGAAAAAGGAAAAGGTA
AAATCCCCAGAAAGTACACTGATATTTAATATTGATCTCTGGAGATTCGAAATGGACCAAGATCCCATGAAT
CATTCGAAGAAATGGATCTTAATGATGACTGGAACCTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGT
TTGAAAACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAGAAGATG
AAGACAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTATAGAGATACATCTACCCCTT
TTAATATAGCACTCATCTTTCAAGAGAGGGGAGTCATCTTTAAAGAACATTTTATTTTATACAAATGTTCTTTCT
TGCTTTGTTTTTTTATTTTATATATTTTTCTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTT
CTTTCTGATAAGTTATTGGGAAGAAAAGCTAATTTGGTCTTTGAATAGAAGACTCTTGACAAATTTTCACTTTC
ACAGATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACCACGACATGA
GACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTCTCCAAGTTAGAGGTCACATTT
GAAAAGCCCTTTGCAATAGCCCAAGGCTTGCTATTTTCATGTTATATGAATAGTTTATGTGTAAGTGGCTCTG
AGTCTCTGCTTGAGGACCAGAGGAAAATGGTTGTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGAT
GTGCAATGCTGAAGTTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAATCCAGCACTTTGGGA
GGCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACAGGAGAAACCCCTATCTCTAC
TAAAAATACAAAGTAGCCCGGCGTGCTGATGCGTGCTGTAATCCAGCTACCCAGGAAGGCTGAGGCGGCAGAA
TCACTTGAACCCGAGGCGGAGGTTGCGGTGAAGCCGAGATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAGAA
AAGAACACGGTTAATACCATATNAATATGTATGCATTGAGACATGCTACCTAGGCAATTAAGCTGATGAAGCTTGG
CTCTAGTGATTGTTGGGCTTATTATGATATAATAGGACAAATCATTTATGTGTGAGTTCTTTGTAATAAATGTA
TCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTACTTCTTAAGGCTAGCGGAATATCCTT
CCTGGTTCTTTAATGGGTAGCTTATAGTATATTATACTACAATAACATTGTATCATAAGATAAAGTAGTAAACCA
GTCTACATTTTCCCATTCTGTCTCATCAAAAACGAAGTTAGCTGGGTTGTTGGCTCATGCCCTGTAATCCCAG
CACTTTGGGGGCCAAGGAGGGTGGATCACTTGAGATCAGGAGTTCAAGACAGCCTTGGCCAACATGGTGAAACCT
TGCTCTACTAAAAATACAAAATTAGCCAGGCGTGGTGGTGACACACCTGTAGTCCAGCTACTCGGGAGGCTGA
GACAGGAGATTGCTTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAGATTGTGCCACTGCACCTCCAGCCTGGG
TGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGACAGACCTACAGCAGCTACTATTGAATAAATACCTA
TCCGGGATTTT

384/550

FIGURE 384

MRLFLWNAVLTLFVTSLLGALIPPEVKIEVLQKPFICHKRTKGGDLMLVHYEGYLEKDGSLF
HSTHKHNNQPIWFTLGILEALKGWDQGLKGMVCVEKRKLIIPPALGYGKEGKGKTPPESTLI
FNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVEDIFD
KEDEKDKGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

385/550

FIGURE 385

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTCGCTGCTGCT
CCAGGTTATGAAGCCTTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGCTGTCC
CTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGTGGG
ATCCTCTTCTCTCGGTGCTCTTGGCACCATCTATGCAGAAGAAGGCCAGGAGACAATGAAG
GGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCTGTGGAACTC
ACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAGTCTTTA
CTGATCTCTCTGTTCTGCTCTTCCAGGACCTGCTGTCTCCCTCCCTCTCTCCACCTTCCAG
CCTCTGGCTACAACACGCTGACGCCAAGGCMAAAGCTCAGCAAACCCAGCCCCAGGATTG
ACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGGGCTGAGGCC
CCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACACAGGAACCTCT
CCTCACCCAGCGACTCTCCTCTGTCAGGGAGCTCCCGCCCCCATGACAGTGGACTCCACC
TCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGGGTGTCCATCCCG
ATGGTCCGCATACTGGCCCCAGTCCCTGGTGTCTGCTGAGCCTTCTGTACGCCGAGGCCCTGATC
GCCTTCTGACGCCACTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCACGGAGACACAGAGG
AACGAGAAGTTCTGGCTCTACGCTTGACTGCGGAGGAAAGGAAGCCCTTCCAGGCCCTT
AGGGGGGACGTGATCTGATGCTCTCCCTCCACATCTGAGGAGGAGCTGGGGCTTCTCGAAG
TTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGTGAAGCAGTATGGCTGGC
TGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAGTCCAGCTGCCCGGACTCC
AGGGCTCTCCCCAGCCTCCCGAGGCTCTCCTCTTGATGTTCAGCCTGACCTAGTGGCGCTTT
GTCAGCCCTGGAGCCACAGAGCGGTGGCTTGTCTTCCGGCTGGAGACTGGGACATCCCTGAT
AGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCAGCAGGGCCAGACAAGGCTCAG
TGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGCCATGCCAGTGTCCGGACCTT
GCCTTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCCTGGCGTCTCAGACTTAGTCCCA
CGGTCTCCTGCATCAGCTGGTGTGAAGAGGAGCATGCTGGGGTGGAGTGGGATTCTGGCTT
CTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCTGTGAAAAACGTGATTCTGGGCCCA
CCAAGACCCACAAAACCATCTCTGGGCTTGGTGCAGGACTCTGAATTCTAACAATGCCAGT
GACTGTGCACTTGAGTTTGGGGCCAGTGGGCCTGATGAACGCTCACACCCTTACGCTAG
AGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCCAATAGATCTGCTGTCTGCGACACCA
GATCCACGTGGGACTCCCTGAGGCCCTGCTAAGTCCAGGCCCTTGGTGCAGGTGCAGTGCATC
TCAGGATAAGCCAGGACCGGCACAGAAGTGGTTGCCTTTNCATTGTGCCTCCTCGGNCA
TGCCCTCTTGGCTTTGGAAAAAATGATGAAGAAAACTTGGCTCCTTCTTGTCTGGAAGGG
TTACTTGCCTATGGGTCTCTGGTGGCTAGAGAGAAAAAGTAGAAAAACGAGTGCACGTAGGTGT
CTAACACAGGAGAGTAGGAACAGGGCGGATACCTGAAGGTGACTCCGAGTCCAGGCCCTG
GAGAAGGGGTGGGGGTGGTGGTAAAGTAGCACAACCTACTATTTTTTTTCTTTTCCATTATT
ATTGTTTTTAAGACAGAATCTCGTGTCTGCTGCCAGGCTGGAGTGCAGTGGCAGCATCTGCA
AATCCGCTTCTGGTTCAGTGTATTCTTCTGCTCAGCCTCCGAGTAGCTGGGATTACAG
GCACGCACCACCACCTGGCTAATTTTTTGTACTTTTAGTAGAGATGGGGTTTCCACATGTTG
GCCAGGCTGGTCTTGAATCTCTGACCTCAATAGGCCTCCTGCTTACGTCTCCCAATTTGCCG
GGATTACAGCATGAGCACTGTGCTGGCCCTATTTCCTTTAAAAAGTGAATTAAGAGTTG
TTCAGTATGCAAACTTGGAAAGATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCA
TAGTCTCACCAGACATCATATTTCGTTTTGTTGTAATCTCTCCACATCTTTCTCTCTC
ACATAATTTTCCGCTGTTCTTTTACAGCAATTATCTGTATATACAACTTTGTATCTCTGC
CTTTTCCACCTTATCGTTCCATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTT
ATAAATAAATGTTTCATCAGCTGCATAAAAAAAAAAAAAA

386/550

FIGURE 386

MRLLVLLWGCLLLPGYEALEGP EEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCSG
TIYAE EEGQETMKGRVSI RDSRQELSLIVTLWNLT LQDAGEY WCGVEKRGPD ELLISLFVFP
GPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPGTSQ
YGHERTSQYTGTSHP PATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRILAPV
LVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAAEKEAPSQAPEGDVISM P
PLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

387/550

FIGURE 387

GC GCGCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCCGCACATG
GCTGCAAGCCACCTCGCGCGCACCCCGAGGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGAGG
CGCCCGGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATCGGG
ATGTCCTCCTCCTCTCTCTCTTGTAGTTTCCTACTATGTTGGAACCTTGGGGACTCACACT
GAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGCTTCCA
GAAAAAGACACTCTGGATATTGAATGGTGCTCACCGATAATGAAGGGAACCAAAAAGTGGTG
ATCACTTACTCCAGTCGTCTATGCTACAATAAATTGACTGAGGAACAGAAGGGCCGAGTGGCC
TTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGCCCAAGTGAT
GAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCATGTCATCTTA
AAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGACAGAAGGAAGT
GACCTGACTTTGCAGTGTGAGTCATCCTCTGGCAGAGAGCCATTGTGTATTACTGGCAGCGCA
ATCCGAGAGAAAGAGGGAGAGGATGAACGCTGCCTCCCAATCTAGGATTGACTACAACCAC
CCTGGACGAGTTCTGCTGCAGATCTTACCATGTCCTACTCTGGACTGTACCAGTGCACAGCA
GGCAACGAAGCTGGGAAGGAAAGCTGTGTGTGCGAGTAAGTACAGTATGTACAAAGCATC
GGCATGGTTGCAGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTGATTTCTCTTGGTG
TGGCTGCTAATCCGAAGGAAAGACAAGAAGAAGATGAGGAAGAGAGAGACTCAATGAAATT
CGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTGTGAAACCCAGCTCCTCTCTCTCAGGCTCT
CGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAAATAGTCCTCACGCGCCAG
CGGACACTGTCAACTGACGCGAGCACCCGAGGGCTGGCCACCCAGGCTATACAGCCCTAGTG
GGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATGCTAATCTGACCAAGCAGAA
ACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAAACGGCT**TGA**ATTACAATGGAC
TTGACTCCCACGCTTCTTAGGAGTCAGGGTCTTTGGACTCTTCTCGTCATTGGAGCTCAAGT
CACCAGCCACACAACCAGATGAGAGGTCACTTAAGTAGCAGTGAGCATTGCACGGAACAGATT
CAGATGAGCATTTTCTTTATACAATACCAACAAGCAAAAAGGATGTAAAGCTATTCACTCTGT
AAAAGGCATCTTATTGTGCCTTAGACCAGAGTAAGGGAAAGCAGGAGTCCAAATCTATTGT
TGACCAGGACCTGTGGTGAGAGGTTGGGGAAAGGTGAGGTGAATATACCTAAAACTTTTAAT
TGGGGATATTTGTATCAGTGCTTTGATTCACAATTTCAAGGAAATGGGATGCTGTTTGT
AAATTTTCTATGCATTTCTGCAAACTTATTGGATTATTAGTTATTTCAGACAGTCAAGCAGAAC
CCACAGCCTTATTACACCTGTCTACACCATGTACTGAGCTAACCACTTCTAAGAACTCCAAA
AAGGAAACATGTCTTCTATTCTGACTTAACCTCATTGATTAAGGTTTGGATATTAAAT
TCAAGGGGAGTTGAAATAGTGGGAGATGGAGAAGAGTGAATGAGTTTCTCCCACTCTATACTA
ATCTCACTATTTGTATTGAGCCCCAAATAACTATGAAAGGAGACAAAATTTGTGACAAAGGA
TTGTGAAGAGCTTTCCATCTTCATGATGTTATGAGGATTGTGTGACAAACATTAGAAATATATA
ATGGAGCAATTGTGGATTTCCTCAATCAGATGCCTCTAAGGACTTCTCTGCTAGATATTT
CTGGAAGGAGAAAATACAACTGTCTATTTATCAACGTCCTTAGAAAGAAATTCCTCTAGAGAAA
AAGGATCTAGGAATGCTGAAAGATTACCAACATACCATATAGTCTCTCTCTCTCTGAGAAA
ATGTGAAACCAGAATTGCAAGACTGGGTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTA
ATATGTCAAGGAAGGTAGCCGGGCATGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAG
GTTGCASTGAGCCGAGATTATGCCATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

388/550

FIGURE 388

MSLLLLLLLLVSYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKVV
ITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHVIL
KVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRIDYNH
PGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLIFLLV
WLLIRKDKERYEEEEERPNEIREDAAEPKARLVKPPSSSSSGSRSSRSGSSSTRSTANSASRSQ
RTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Important features:**Signal sequence:**

amino acids 1-16

Transmembrane domain:

amino acids 232-251

389/550

FIGURE 389

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTCG
CCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCAGATGCACCCCTGT
CCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCCCCA
AAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTACTCA
GCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGGAGAAC
AGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGAATGTGA
CAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAGTTTATTC
AGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCACAGACTGA
ATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACATGAAATTCA
GGTCTAGCTGGGTATTTATTGCAGCAAAAAGGCTTGGAAGTCCCTTCCGAAATTCAGAGAGAAA
AGATCAACCACTCTGATGCTAAGAACAACAGATATTTCTGGCTGGCCTGCAGAGATCCAGATAG
AAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCCTGAGTAAATGTGTTCTGTATA
AACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCACAGCCCATATTTGAT
GAGTATTTTGGGTTTGTGTGAACCAATGAACATTTGCTAGTTGTATCAAATCTTGGTACGCA
GTATTTTATACAGTATTTATGTAGTGAAGATGTCAATTAGCAGGAACTAAAATGAATGG
AAATTCTTAAAAA

390/550

FIGURE 390

MRPLAGGLLKVVVFVFSALCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQKC
DHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTATRC
FDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRSSWV
FIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Important features:**Signal sequence.**

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

391/550

FIGURE 391

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGGCTCGGAGGGGTGCGCGGGAAAGGG
 AGGGAAAGGAAGGGCGGGGGCGGGCCCGCTCGCGCCCGCCCGCGGCTCTGTCGGCGCCCTGTCCGCCCGCGGCC
 AGCCAGCCCGACGCGCGGGCGCGGTCAACAGCGCAGCGCGCGCGCTTCCCGCGCCAAAGCGCGCGCTCTG
 CTGTGCGCTGCGCGCTTGCCTCGCGCGGCTGTCTGCGCCGCGACCGCGCGCGCGCGCTGACCTGTACCT
 GCGCTGCGCGCGGGCGGAGAGTGTCTCCCGCGGGGACCGCTACCCAGCGCTGCGCTGTGTGTCTGCTGCG
 AGTGACCTGTGCGGGTTCGGAGCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGCGAGGAGATCTGGAG
 CCGGAGGCCCTACTACGCGCGCCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCTGCGGGCGCGGGGA
 GGAAGTGGAGCGCGCGCGCGAGGCCAGGCCCGCCAAAGAGGGCCACCAAGCCAAAGAAAGTCCCAAGAGGGGA
 GAAGTCGGCTCCGAGGCCGCTCCACACAGGTAAACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAA
 GGCTGCCAACGATGATCAGAGTGTCCGTGTGGCCGTGAAGATGTCAGAGAGAGTTGCCACCTCTTGTCTGGA
 AACCTTAAAAATCAGAGACTTCCAGCTCCATGCTCCACGGTGAAGCGCTATGGCGCTGGGGGCACATCGAGGGAG
 ACTCAACATCCAGCGCGGCTATTAAATGAAATGATTTTATGACGGAGCGCTGTTGCGCGGGAAGAAATGACCTCCA
 GCGATGGATTGAAGTGGATGCTCGGGCGCTGACAGATTCTAGTGTGTCATCACTCAAGGGAGGAACCTCCCTCTG
 GCTGAGTGACTGCGGTGACATCCTATAAGGTCTAGGTGAGCAATGACAGCCACACGCTGGGTCACTGTTAAGAAATGG
 ATCTGAGAGCATGATATTGAGGGAAACAGTGAGAAAGAGATCCCTGTTCTCAATGAGCTACCCGCTCCCATGCT
 GCGCCGCTACATCCGCATAAACCTCAGTCTGTGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCTGGG
 CTGCGCACTGCCAGATCCTAATAATTATCACCAGCGGACGAGATGACCACTGATGACCTGCGATTTTAA
 GCACCAATTTATAGGAAGTTGCGCGAGTTGATGAAAGTTGTGAATGAAGTGTGCCAATATCACCAGAAATTTA
 CAACATTTGGAAGAAAGCCACAGGCTGAAGCTGTATGCTGTGGAGATCTCAGATCACTCCGGGAGGATGAAGT
 CGGTGAGCCGAGTTTCACTACATCGCGGGGGCCACCGGCAATGAGTGTCTGGCGCGGAGCTGCTGCTGCTCT
 GGTGCACTTGTGTGTGAGGATGATTTGCCCGGAATGCGCGCATCTGCCATCTGTGGAGGAGACGCGGATTCA
 CGTCTCCCTCCCTCCCTCAACCCGATGGCTACGAGAAGGCTACGAAGGGGGCTCGGAGCTGGGAGCTGTGCTCCT
 GGGAGCTGGACCCAGTGGAAATGACATCAACAACACTTTCTGTATTTAAACACGCTGCTCTGGGAGGCGAGA
 GGAATGCAAGATGTGCCACAGAAAGTCCCAATCACTATATTGCAATCCCTGAGTGGTTCTGTGCGGAAGATGC
 CACGCTGGCTGCCGAGCAGGACGTATAGCTTGATGGAAAAATCCCTTTGTCTGGCGCGCACTCA
 GGGCGCGAGCTGTGTGTGCGCTATCCCTACGACCTGGTGGCTCCCTTGGAGAGCGCAGGAACACACCCCCAC
 CCGCGATGACACGCTGTTCGCTGGCTGGCTACTCTATGCTCCACACACCGCTCATGACAGAGCGCCGGAG
 GAGGGTGTGCCACAGGAGGACTCCAGAAGGAGGAGGGCACTGTCAATGGGGCTCTGGGCACACCTGCGTGG
 AAGTCTGAACGATTTCACTACCTTATACAAATGCTTCAAGATGTCCATCTACGTGGGCTGTGATAAATACCC
 ACATGAGAGCGAGCTGCCCGAGGAGTGGGAGAATAACCGGAATCTCTGATCGTGTTCATGAGCAGGTTTCACTG
 TGGCATTAAAGCTTGGTGAGAGATTCAATGGAAGAGGAATCCCAACCGCCATTATCTCCGTAGAAGGCTTAA
 CCATGACATCCGAACAGCCAACTGAGTGGGATTACTGGCGCTCTGAACCTGGAGAGTATGTGTCACAGCAAA
 GGCGGAAGTTTCACTGATCCACCAAGAACTGTATGGTGGCTATGACATGGGGGCCAAGAGTGTGACTTCAAC
 ACTTAGCAAAACCAATGCGCAGGATCCGAGAGATCATGGAGAAGTTTGGGAAGCAGCGCTCAGCTGCTGCGAGC
 CAGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGCTGGGTCAGACCTCTGGGCGCTTGAGACTGCTCTGGG
 ACCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAGTGGACTCACTCACTGTGTTTCTCTGTAATCAAG
 AAGTCTCGGAAGAGAGGGTGCATTGTGAGGCGAGTCCCAAGAGGAGGCTGGAGGCTGAGGCTGTCTTCTTT
 CTTGTTTCCATTATCCAAATTAATTTGACAGAGCAGCAGCAAGAGCTGATGGGAGTGAGAGAACTCAGCAAG
 CCACCTGGGAATAGAGAGAGAGAGAGAGAGGAGGGGAGCTGTGCTGCTGAGCGCTCTGCTGAGAAAGG
 ATTCTGTGCTCTCCCTGTGTGCTGGCAGCAAGGGTTCCAGTGCATTTGCAATTTGACAGCTTAAATTTGAG
 CATTTCGCCAGCTGGGCTGCCCAATGTTACCAATTTGAGATGCTCCAGGCGCTCAAGAGAATCCACCTCTC
 TGGCGCTGGGACATGCAAGCTGCTACAATAAATCTCTGTCTTTTGAACAAAGGAGTGTTCAGAAAGGAGAGGCTGGA
 TCACTGAGGCTCTTGAATCTGTTAGTCTCTTTTCAACAAGGAGTGTTCAGAAAGGAGTGTGCGAGGCTGGA
 GATCATCTCAGGAGTTTGTGGGCGCAAGCATGGAGCTTCTTGACAAATCTGGGTCCATAAACAACCGCCAAA
 GTCCCTGCTGATCCAGTACCCCTGAGAGTTCGCCAGTAGGAGAGAGCAGAGTGTGCCCTTCTGAGAGGCCA
 GAAATTTAGCTGGATCTCTCTTTTACCTGCTAGGACTGGAAAGAGCCCAAGTGGGCTGGCTGAGGCCCTCTC
 TCTGCTGTGAGGATTTGCCCGTGTGTGGAATGAGTGCTATGGGTGGGCTCATATCAGCCTGGGAGTATT
 TTGATGTAGAAATGCCAGATCTCCAGATTAGCTAAATGTAATGAAACCTTATAGGATTAATCTGTGGAGCAT
 CAGTTTGGGAAGAAATTTGAATTTATCTTCCAAGAAAAAGTATGTCTCACTTTTGTTAATGTTGCTGCTCAT
 TGACCTGGAAAAATGAAAAAATAAAGCAAAATGGTAAAGCCCTTACAAAAAATAAATAAATAAATAAATAA

392/550

FIGURE 392

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPFYARPEPELETFSPPLPA
GPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSEKAANDDH SVR
VAREDVRESC PPLGLET LKITDFQLHASTVKRYGLGAHRGR LNIQAGINENDFYDGAWCAGRN
DLQQWIEVDARRL TRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIFEGNS
EKEIPVLNELPVPMPVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTTDDLD
FKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGA
HGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGGSELGGWS
LGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAAETRAVIAW
MEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRLAYSASTHRLMTDARR
RVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELS IYVGCDKYPHESQLPEEWENNR
ESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKA
EGFTASTKNCMVG YDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARRLKLGRKR RQRG

393/550

FIGURE 393

GTCCACATCTCTGCTCAACTGGGTGAGGTCCCTCTTAGACACAGCTCTTGTGTCATCATTTGCTGAAGTGGACCAAC
 TAGTTCCTCCAGTAGTGGGGGTCTCCCTTGGCAATTCTTGATCGGGCTTTGGACATCTCAGATCGCTTCCAATGAAGA
 TGGCCTTGGCTTGGGGTCTGGTGTATTTCATAATCATCTAACTATGGGACAAGGTTGTGGCGGGCAGCTCTGGGGGG
 AAGGAGCAGCGGGCTGATCAGAGCATCTCAGGAACACTGGAGGACTTGTCCAGCCTTGAAGAAGACTTAGTGGTT
 TCTGAATCTAGCCACTTTGGCGGTAACTGATGCAACTCTGCAACTTCTGCTGGGGCTTTGGGGCCAGGTTGG
 CTACTTATTTCTTTTAGGGGATGTGTCAGGAGGTGACCACTCTCACGGTGAATACCAAGTGTGTCAGAGGAAGTGCC
 ATCTGTGTACAGTGATGGGAGAGCTGTCCAGGAACCTGGGCGGGAGGAGAGGCGGAGGCTGCTGGGGCGGCTT
 CCAGGTTGTGACAGTCTGCTCAGGCGCTCCCATTACAGTGGACTCTGAGGAAGGCTTGTCCAGCAGGAGGCGG
 GCTGGATCGAGAGCAGCTGTGCGGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTGCCACAGGGGATTT
 GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACAGCCAGCCAGTTTCCAAAGGCGAGCAGGA
 GCTGGAATCTCTGAGAGCGCTCTCTGCGAACCCGATCCCCCTGGACAGAGCTCTTGACCAGACACAGGCC
 TAACACCTTGCACACTACACTCTGTCTCCAGTGAGCACTTTGCCTTGGATGTGCTTTGGGGCCCTGATGAGAC
 CAAACATGACAGACTCATATGTTGTAAGGAGCTGGACAGGGAATCCATTCTTTTGTATCTGGTGTAACTGC
 CTATGACAAATGGGAACCCGCCAATCAGGTACCGATCTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG
 CCCTSGCTTTGCTGAGAGTTCACTGGCACTGGAATCCAAGAGATGCTGCACCTGGTACGCTTCTCTAATAAAT
 GAGCGCCACAGCCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCAACTGCTCCAGAGGT
 GCTGGACACTCTCAGATTGATGCCAGACAGGCGAGGTCACTTGGGTCGACTCTAGACTATGAAAAGAACCC
 TGCTCATCAGAGGTGGATGTTCAGGCAAGGAGCACTGGGTCCCAATCTATCCCAAGCCCAITGCAAAAGTTCTCATCA
 GGTCTTGGATGTCAATGACACATCCAGACATCCAGTCATCCGCTCCAGCCATCAGCTGGTGTGCAAGG
 TCTTCCCAAGGACAGCTTTATGTCTTGTGATGGCAGATGACTTGGATTCAGGACACAATGGTTTGGTCCACTG
 CTGGCTGGCCAGAGAGTTGGGCCCTCTCAGGCTGAAAAGAACTAATGGCAACATACATGTGCTAACCAATGC
 CACACTGGACAGGAGGAGTGGGCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
 AGCCAGAGAACAGCTCAGACTTCAATCAGTGCATCAACGACATGACCTGTGTTTGAAGAAGGAGGATGTA
 AGTCTCCAGCGGGGAAACAACTTACCCTCTCTTCACTTACCTTACCATCAAGGCTCATGATGTCAGACTTGGGCAT
 TAATGGAAAGTCTCATACCGCATCCAGGACTCCGAGTTGCTCACTTAGTAGCTTAGTACTGCAACACAGCAGGA
 GGTCACTGCTCAGAGGTCACCTGAACATATGAAGAGATGCGCGCTTGTAGTTCCAGTGATGCCAGAGGACAGCGG
 GCAACCCATGCTTGCACTCCAGTGTCTTGTGTGGGTGACGCTCTTGGATGCCAATGATAATGCCCAAGAGGTGGT
 CCAGCTGTGCTCAGGCTATGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCTCCACAGGCACTGCTGGTGGCC
 CTTCTGAGACTCCCAATGGCTTGGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCAGAGCTCCCGGCCATT
 CATTTTGACAACCAATTGTGGCAAGAGATGCAACTCGGGGGCAAAATGAGAGCCCTCTACAGCATCCGCAATGG
 AAATGAAGCCCACTCTTCTATCTCAACCTCTATACGGGGCAGCTGTTCGTCAATGTACCAATGGCCAGAGCT
 CATTGGGCTGAGTGGGAGCTGGATAGTAGTAGAGGACAGGAGGCCCCCTTACAGACCCGAGGCTTGT
 GAGGTTGATGTTGTGACAGTGTGGACCACTGAGGACTCAGCCGCAAGCTTGGGCTTGGAGCATGTGAT
 GCTGACGCTGATCTGCTGAGCTGATCTTGGGCACTTCCGGTTGATCTTGGCTTGTTCATGTCCATCTGCGG
 CACAGAAAAGGAGGACCAAGGCCCTCAACTCTGCGGAGGCGGAGTCACTTACCGCCAGCAGCCCAAGGAGGCC
 CCAGAAACATTTCAAGAGGACGACATCACTCTGCGCTGTGCTCAGGGCTCAGCAGGTTGAGCTTTGTGAAT
 CGGGCAGTCCCAAAAGATGTGGACRAGGAGCGATGATGGAAGCAGGCTGGGACCCCTGCTGCAGGCCCTT
 CCACCTCACCCGAGCTGTGACAGAGCCTGCGTATCAAGGCAACAGGAGGAGCCGCGGAGGAGGAGAGGT
 GCTGAGACAGGCTGAACCTCTTTCAAGCATCCAGGACAGAGGATGCTTCCGCGGAGCACTGAACTGAACTTCC
 CGAGCCCAAGCTGCCAGGCGCAGCCAGTTCAGGCCCTGGAAGTTTGCAGGCAAGCCCAAGGAGGAGGCTGGC
 TGGAGACAGGCGAGTGAAGGAGCCACAGAGGCCACAGGCTCTCTGCAACCTCTGAGACGCGACGACATCT
 CAATGGCAAGTGTCTCTGAGAAGAATCAGGGGCCCTGATGATCTGCGAGGCTGGTGGCGGTGTCTGTGGC
 TGCCCTTCGCGAGGAGCCCGGTGGAGGAGTCACTGTGATTTCTCTCTGCTTACGAAATCTCCAGGCTGCT
 GTCTTGTGCTGATCAGGGCCAAATTCAGGCCAAACAAACACAGGAGAAATAGTACTTGGCCAGGCCAGGAGG
 CAGCAGGATGCAATCCCAAGACAGATGGGCCAAGTGCAGAGGCTGGAGGCCAGCAGACCTCGAAGAGGAGA
 AGGGCCCTTGGATCTCTGAAGAGGACTCTGTCTGAAGCAACTGCTAGAAGAACAGCTCTCAAGTCTGCTGCAC
 CAGCAGAGTCTGGCCCTGGAGCCTGTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTTTTGGCCCTCAC
 CCAACACTACCGTGACATGTGATCTCCCGGATGCTGACAGCCAGGAGAGGCGGAGGACTTCCAGAGCTTCCG
 CAGGCGAGAGGCCACAGAGCTGAGCCCAACAGGCACAGGCTGGCGAGCAGCTTTGTCTCGGAGATGAGCTCAT
 GCTGGAGATGCTGTGGAAGACAGCTCCAGCATGCCGCTGGAGGCCGCTTCCGAGGCGCTCGCGGCTCTCGGT
 CTCCGGGAGGACCTCTAGTTTAGACTTGGCTCAGAGTGCAGCTCAGGCATGAAGTGCAGAGGAGCCAGGTGG
 AAGAGCGGGACTGAGGGCAGAGGACAGGCAAGCAGCAGCAGCAGGCTGCTCTGACACATACTCAGACGCT
 CTGGATTCAGAGAAACAGGGGCTPAGGATCTGTGGACAGAGCTGGTTCTTAAAGATCTTGAATCACTAGCTAG
 CGCGGCTCTGAGAACTTTAGGTTGACTGATGCTATCCCAAGAGGAGGACAGGCCCCAGGACTAACAGCTGAC
 TGACCAAGCAGGCCCTTGTAGCAGCTCTGAGTCTTTTGGAGGACAGGAGCGGCTTTTGGCTGAGATAGTGT
 TCTTGGCAAAACATATGTGAGCACAAAGGGTCAGTCTCTGCCAGAACAGATGCCACGGAGTATCAGGCCAGG
 AAAGGTGGCCCTTCTTGGGTAGCCAGGATCAGGGGCTGTACCCCTGGGCGTGGCAGGAGTGTCTCTGACCTAT
 CATTAAGGAAAAGCAGTAAAAAANAANAANAANA

394/550

FIGURE 394

MMQLLQLLLGLLPGGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQAG
 AAFQVLQLPQALPIQVDSEGLLSTGRRLDREQLCRQWDPCLVSFVLTATGDLALIHVEIQVL
 DINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGFNTLHTYTLSPSEHFALDVIVGPD
 ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESSLALE
 IQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPLDYEKN
 PAYEVDVQARDLGPNPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSFIALVMA
 DDLDSGHNGLVHCVLWSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQDQGLQPLS
 AKKQLSIQISDINDNAPVFEKSYEVSTRENNLPSLHLITIKAHADLGLNGKVSRYRIQDSPV
 AHLVAIDSNTEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMCLASSVSVVWSLLDANDNAPEVVQ
 PVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTTIVARDADSGA
 NGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGSFPPLQTRALLRV
 MFVTSVDHLRDSARKPGALSMMLTIVICLAVLLGIFGLILALFMSICRTEKKDNRAYNCREAE
 STYRQQPKRPQKHQIKADIHLPVLRGQAGEPCEVGQSHKDVDEKAMMEAGWDPCLQAPFHLT
 PTLYRTLNRNGNQGAPAESREVLQDTVNLLFNHPRQRNASRENINLPEPQPATGQPRSRPLKV
 AGSPTGRLAGDQGSEEAQORPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAFAE
 RNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKPGGSRSAIPDTDGPSARAGG
 QTDPEQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPDPAWMARLSPLTTNYRD
 NVISPDAAATEEPRTFQTFGKAEPESPTGTRLASTFVSEMSSLEMLLEQRSSMFVEAASE
 ALRRLSVCGRTLSLDLATSAAAGMKVQGDPGGKTGTEGSRGSSSSSRCL

Important features:**Signal peptide:**

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

395/550

FIGURE 395

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAGG
CTCCAGAATCGTGTACCAAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAATC
AGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGTGCG
GCCAAGACGPGGATGTTCTTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGCACAG
GAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGGCCTTG
TTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCCTTACAGCT
GCCCCACTGTAAAAAACC GAAATACACAGTACGCC TGGGAGACCACAGCCTACAGAATAAAGAT
GGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGAT
GTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCCCTGGGGTCC
AAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCA
GGCTGGGGCACTGTCACCAAGTCCCCGAGAGAATTTTCTGACACTCTCAACTGTGCAGAAGTA
AAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGTC
TGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCTGGTGTGT
GATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGAGGTCCGACAAACCT
GGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGC
TGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCTCTGGTTC

396/550

FIGURE 396

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLV
GGNWVLTAAHCKKPKYTURLGDHSLQNKDGPEQEIPVVQSIHPHCYNSSDVEDHNHDLMLLQL
RDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTLNCAEVKIFPQKKCEDAYP
GQITDGMVCAGSSKGADTCQGDSSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLDWI
KKIIGSKG

Important Features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

397/550

FIGURE 397

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTCGGACCTGCTAC
TACTGGGCCGTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGGGT
ACTCAGGGCTACTGGCTGGGGTGGAAAGTGAAGTGTGGGTACCCCCATCCGCAACGTCACTG
TGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGCTGCA
GCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCACATGGTGCCCCCTG
ATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCCCTGAGC
TCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGCCATGTGG
TGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCGCCGTGTCCATC
CTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGGAGATCTACC
AGGAAGACCAGATCCATTTCTATGTGCCACTGGCACGGCAGGAGACTTCTATGTGCCTGAGA
TGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCAGGTGGATGGCA
CAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAAGCTGGCAGCCGGG
AGACTTCAGTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGATGACGGTGACACCC
GCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTGAGGAGCTGGACTTGG
AGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGCCCTGGGACTACCA
AGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAGTAACCCCATGGCCTGCACCTCC
TGCAGTGCAAGTTGCTGAGGAAGTGAAGAGACTCTCCAGCAGACTCTCCAGCCCTCTTCTCCT
TCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGCTCCAGCCCTCTTGCTAAG
CCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCAGGACTATTTTCTGCACCA
GCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTCACAGTGGAGCTTCCAGGACC
CAGAATAAGCCAATGATTTACTTGTTCACCTGGAAAAAAAAAAAAAAAAA

398/550

FIGURE 398

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGRL
FTESCSISPKLRsIAVYYDNPHMVPPDKRCrCAVGSILSEGEESPSPELIDLYQKFGFKVFSFP
APSHVVTATFFYTTILSIWLATRRRVHPALDtyIKERKLCAYPRLEIYQEDQIHfMCPLARQGD
FYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSFPGSRETSaatLSPGASSRGW
DDGDTRSEHSYSESGASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTApeKGKE

400/550

FIGURE 400

MSNSVPLLCFWSLCYCF AAGSPVPFGPEGRLDKLHKPKATQTEVKPSVRENLR TSKDPEHEG
CYLSVGHSQPLEDCSFNMTAKTFFIIHGWMSGIFENWLHKLVSALHTREKDANVVVDWLPL
AHQLYTDVAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTVGRI
TGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDFQPGC
GLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS CRKNR
CNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:**Signal peptide:**

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

401/550

FIGURE 401

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCTG
CCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCTGT
CAGTTTCCCAGACAGTCCCTGGCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGGCTC
AACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCCTGGTACC
AGCAGCGGGCAGGCAGTGCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCACCACC
GGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAAATGCCTGTGTCC
TCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGCTACGGCT
TTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCTGCCCTGA
CCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGGTTAATAATA
TTCAACATGTCAACAAC

402/550

FIGURE 402

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGS
APRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSF

403/550

FIGURE 403

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGCGCGTGCAGCAGCTCCAGAAAGCAGCGAGTTG
GCAGAGCAGGGTGCATTTCCAGCAGGAGCTGCGAGCACAGTGTGGCTCACAAACAAGATGCTCAAGGTGTCAAGC
CGTACTGTGTGTGTGTGCAGCGCGCTGGTGCAGTCACTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGG
GCGGTGCGGACGGCGGTAATTTTCTGGATGATAAACAAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGG
ACAGTGGAAACAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCCTTCGATCA
GGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTATGCATTTGCTCAAGATTCT
TCAGACTGCAGTCTGCATTAGTACCAGGAGGCTTACACACAGGATGAAAGAAGCAGGAGTAGACCATAGGCAGTG
GAGGGGTCCCATATTATCCACCTGCAAGCAGTGGCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCA
TACCTACTCTTTTCAGTGCAAACTAGAATATCAGGCAATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGG
ACATTGCCCATGTCTTCAGATAAGCCCACCACTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCTGGAGTT
CAGGGAAGTGGCAACAGATTGCGGGACTGGTTCAGGGCCCTTCATGAAAGTGGAGTCAAAACAAGAAGACAAA
AACATTTGCTGAGGCGTGAGAGAAGCAGATTTCGATACCAGCATCTTGCCAATTTGCAAGGACTCACTTGGCTGGAT
GTTTAACAGACTTGATACAAACTATGACCTGCTATTGGACAGTGCAGAGTCAGAAAGCATTTACCTTGATAAGAA
TGAAACAGTGTACCAAGGCATTCTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTG
CTACTGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTGAGAAGCGGCAAGGGGTAAA
GAAGTCTCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGCCAACACAATGTCTATGGCAGTGT
TGGACAGTGTCTGGTGTGTGACAGATATGAAATGAAGTCAATGGGATCCAGAATAAATGGTGTGCAGATTGTGC
TATAGATTTTGAGATCTCCGGAGATTTTGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGA
CGATATTATGAATGATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGA
CCATGATGATATACATTGAGTTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTACAAAATGATAG
CCTATTTAAAATATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCAGATATATTTGTATAATATTTGAA
AAATTGCAGCTAAAGTTATAGAATTTATGTTTAAATAAAGAATCATTTGCTTTGAGTTTATATTCCTTACACA
AAAAGAAAATACATATGCAGTCTAGTCAGACAAAATAAGTTTGAAGTGCTACTATAATAAATTTTCACGAGA
ACAAACTTTGTAAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTATGTTAATTTTGTAAAGAT
AATTCTAAGTGAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGGAAAAATATGCATGCT
TTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAGGATAACAGAGAGATACCACATGACTCCA
AAAAAAAAAAAAAA

404/550

FIGURE 404

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFRD
EVEDDYFRTWSPGKFFDQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEAGV
DHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCPCPSDK
PTSTSRNVKRACSDLEFREVANRLROWFKALHESGSQNKKTLLRPERSRFDTSILPICKDS
LGWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQRQQDP
PCQTELSNIQKRQGVKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGSRINGVA
DCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

406/550

FIGURE 406

MTPQSLLTQTTFLLSLLFLVQGAHGRGHREDFRFCQSRNQTHRSSSLHYKPTPDLRISIENSEE
ALTVHAFFFAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYKGRDFLLSDKASSLLCFQHQE
ESLAQGFPLLATSVTSWWSPQNISLPSAASFTHSFHSPHTAAHNASVDMCELKRDQLLSQF
LKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQDLHIH
SRQEEEEQSEIMEYSVLLPRTLFPQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGEKVLGI
VVQNTKVANLTEPVVLTFOHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRRETQTSCF
CNHLTYFAVLMVSSVEVDVAVHKHYLSLLSYVGCVVSAACLVITIAAYLCSRVP LPCRKRPRDY
TIKVHMLLLAVFLLDTSFLLSEFVALTGSEAGCRASAIFLHFSLLTCLSWMGLEGYNLYRLV
VEVFGTYVPGYLLKLSAMGWGFPFI FLVTLVALVDVDNYGPIILAVHRTPEGVIYPSMCWIRDS
LVSYITNLGLFSLVLFNMAMLATMVVQILRLRPHTQKWSHVLTLLGLSLVLGLPWALIFFSF
ASGTFQLVVLVLYLFSIITSFQGLFIFIWYWSMRLQARGGPSPLKSNSDSARLPISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657**Microbodies C-terminal targeting signal.**

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344**G-protein coupled receptors family 2 proteins**

amino acids 475-504

407/550

FIGURE 407

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGAG
CCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTCGC
TCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCTGGA
CTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAAGCCC
TGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAAAGCTC
AGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAGCAGGGC
TCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGCTCAGCTG
CCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTGCTACATGA
CTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGCTTATTTAC
AAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACAACGGGATCTT
CCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAACGTGTGCCGGAT
GTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGCCATGAAGATAAC
CCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCCAGGGAAAAGACCT
CACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCACAGCAGGCTGGGAA
ATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATAAAGGATGGTTGAACG
TGAAA

408/550

FIGURE 408

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALDY
EADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGYWE
AWRHHCQGRDLTEWVDGCDF

Important features:**Signal peptide:**

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

409/550

FIGURE 409

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
 CTCTTTCAGCCCGGGATCGCCCGACGAGGAGATGGGCGACAAAGATCTGGCTGCCCTCCCCGPGCTCCTTCTGGCC
 GCTCTGCGCTCCGGCTGCTGCTGCTGGGGCGCCGCTCACACCTTCCCTTACAGGACTTCACCTTTACCCCTT
 CCCGCCGCCAGAAAGGATGCTTCTACAGCCCATGCCCTCGAAGGCTCCGCTGGAGTCTGAGTCCCAAGTTTGA
 TCGGAGCAGGATATGATATGATTTCATCTTGCCTCGAAGCAAGCAAAACCTTAGTTTGAACCAAGAAA
 TCAGATGGAGTTCACACTGTAGACATGAAGTTGGTGATTACATGTTCTGCTTGTCAATAACATTACGACCCATT
 TCTGAGAGGTTGATTTCTTGAATTAATCTGGATAATATGGGAGAACAGGCACAGAACAGAAAGATTGGAAG
 AAATATATTACTGGCACGATATATTGGATATGAACTGGAAGACATCTCGGAATCCATCAACAGCATCAAGCTCC
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCAITTTGAAGCTCGTGATCGAAACATCAAGAAAGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAITTTAGTGGTCATGGTGGTGGTGTACGCCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTGAAGCTTAAACTCCAAACTAGAGTACGTAACTTTGAAA
 AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAAATATTTTGAGATATA
 AAAGTAGGAAACAGGTATAATTTAATGTGAAATTAAGTCTTCACTTCTGTGCAAGTAACTCTGTGTATCCAG
 TTGTACTTAAGTCTGTAAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCATATTTAATACTGCAT
 TTTCTAATCTTTGAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCTAATTTGCACACCC
 AGTCTGTTTTAACAGGTTCTATTACCCAGAACTTTTGTGAATGCGGCAGTTACAAATTAATCTGTGGAAGTTT
 TCAGTTTAACTTTAAATCACTCGAGAAATACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCGAA
 CTTTTCTCTATTTCACATATGCACTCTCCCTTAATGTAAATAGAATAATAGCTTTGAATATCAATTAGGTTTGTG
 AGATTTTATTAACCAATACATTTTCAGTGTAACTATTACAGAAAGACTTAGTCTTTTGTACTTTCTGTACATT
 CCAAAAGCTGACATTTTCAGGATCTTAAAAACACAAAGTTACACTTACTAAAATAGGACATGTTTCTCTCTG
 AAATGAAGRATATAGTTTAAAAGCTTCTCTCCCAATAGGGACACATTTTCTTAACCTTAACTAAAGTGTAGGA
 TTTTAAAATTAATGTGAGGTAAAATTAAGTTATTTTAAATAGTATCTGTCAAGTAAATATCTGTCAACAGTTAA
 TTAATCACTGTTGTTAATTTTAAATGATGCTGACTTGGATAATTCATTATTAACAGCAGTATTGAAGGAAATA
 TTGCTAAAATGATCTGGGCCCTACCATTAATAAATATCTCCCTTTTCTGAGCTCTAAGAAATATACAGAAACAGGAA
 AGAATTTAGAAAACCTTGAGAAAACCTTAATCCAAAATAAAATTCACCTTAAGTAGAATATTAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCTTACTCATACATAAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
 AAATCTTTGGCTGTAGGTTTTATTTTCTACAAGAAATCTGGTTGAATTTTGTGAAGCAGGTACATTTTATA
 AAATGTAAAGCCCTACTGTAAAGTTTAGCACTGGGTGTACATATTTATTAATAAATTTTATTTATAACAAATTTTAT
 TAAAATGGCCTTTCTGAACACTTTATTTATGTAGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTAA
 CACCTAAATGTGAATAAACCATATATACAAACAAAGTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
 TCAAGTACTAGTAATTTAACTCATCATGAATGAATATAATTTTAAAGTTATGCCATTTTAAACGTTGTGTTAT
 GACTACATTTGTGAGTTAGAAACAAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTAGTAATGCTGGAAT
 CTTGATGAGCACAATGATAACAGAGAGTGATTTCAATTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
 TTTAGGCCCTTGGGAGAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTAAATAAGTGAAGTATGCGGTAT
 ATGATCAATTACCTTAATGGCCAAAGAAATGCTTCAGGTGCTAGCGGTATCTCTGCAACACTTGCAGAACAA
 AGGTCATTAAGATCTTGCCTATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGCAATGAGAAGCAAAATTTACA
 GTACCAATACTAATAAGCAGGATACAGATATAAACTACTGCATCTTTCTATAAACTGTGATTAAGAAATCTCA
 CCTCTCCTGTATGGCTGTACTGTACTGTACTCTGTACTCTTACCTTAACAAATGAATTTGTACATAATCTTCT
 ACATGTATGATTTTGTGCCACTGATCTTAAACCTATGATCTTACCATTCTTACCATAAATAAGCATCTGTTATGCT
 TATTTGGAAGAAATTTAGGAATACTAAGGACAATTTATTTATAGCAAAAGTAAAGACAGATATTTAAGAGG
 CATAACCAAAAAGCAAACTTGTAAACAGAGTAAAAATCTTAAATATTTAGCAACATCTGTTTATCTGCTT
 CATATGCTTTTATTAATTCATATTCATTTCTAAATTAAGGTTATGCTAAATGAGTAAGCTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTTCATATACAAATTTAAAAATACTACAATTTAACTAAGGCCCAACAGGATTC
 CTAATGTAGCTGTTACCGGTGTCACCTCACACTAAGGCCTAGAGTTTGTCTGTATGCAATTTGGATGATTAAT
 GTTATGCTGCTTTTCTATGTAATGTCAAGACATGGAGGTGTTTGTAAATTTATGTTAAATTAATCTTCTTCA
 CACATTAATGGTGCTTTAAAATTTGACAAAAATGAGCACTTACAATTTGATGTCTCTCAATGAAGATCTTCTTAT
 GTGAATTTTAAAAGACATTTGATTCGGCATGTAGGAATTTTCACTGAAGTACAAATATGCACATCACTGTTG
 CTCAAACTGCTTTTACTTTATAAACAGCCATCTTAAATAAGCAACGATTTGTGGAGTACTGATGTATATAATGA
 AAATATCAAGGAAAA

410/550

FIGURE 410

MGDKIWLPPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEYQ
VLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFELIL
DNMGEQAQEEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRNIQE
SNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKRSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

411/550

FIGURE 411

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTCCCAGGGGACCGCATTCCAGAGTCA
 GTGACTCTGGAAGCACCATCACTCACTCTTGGCCAGGTTCCACAGGGCTTGGGGGAAAGATGCTGGGGACCAAG
 GCCTGGGTGTCTCTTCCCTTGGTCTTGGAAATACACATCTGTGTTGGGAGACAGACGATGCTCAACCCAGTCAATA
 AGAAGACTCCAGCTCGGGAAGAGAACCACGACATCTTTGCGACAGCTTCCGACACCTCTGGAGAGCCCTGGTGAG
 TGGACACATGGTTCACATCTGCTACCGCAGCGGGAGGGCATTATGACGGCTGAGGAGCCATCTGCTCTTAC
 TATGGGACCGCTGTATGTGGCCGTCCCTTGGCGGTAGAGGCTCGACACTGACTGGACACTCGGGGACGACT
 GCGCAGGTGGTCTATGGTAGTGCCTCGGGTGGGGTTTCTGGTGGCTCAACAGGGAGCAGCGGGCTGGCCAGAACTGC
 TTTAAATACACGTAAGCTTCTCTCTGCGCCACAGGATCCCTGCGCGAGACACAGAGCCGATCTGGAGGCCATGG
 TCTCCCTGGAGCAAGTGCTCAGCTGCTGTGGTCAGACTGGGGTCCAGACTCCGACACGCAATTTGCTTGGCAGAG
 ATGTGTTGCGCTGTGAGTAGGCCAGCGAAGAGGTCAGCACTGCATGGGCGAGGACTGTACAGCTGTGACACTG
 ACCTGCCCAATGGGCGAGGTGAATGCTGACTGTATGCTGATGTGCGAGGACTTCATGGTTCATGGGGCTGTC
 TCCCTTCCGGAGGTGGCCAGCTCAGGGGCTGCTATCTACCTCTGACCAAGAGCGCGAGGCTGCTGACCCGAG
 ACGACAGTGTATGAGATTCGGAATCTCTGCTTGTGGCTGTAGGCAAGCATCTTGAGATACACAGGTC
 AAGTTTCCCCCATTTGTACTCACATGGCCCAAGACTAGCTGAAGCGACCCACCATCAAGGCAGAGATTTGTGAGG
 CGAGAGACTCCATACATGGTATGAACCTGAGACAAAAGCAGGAGAGCTGGGCGAGAGCGTGTCTGTGTGCTGT
 PGGCCACAGGGAGACCCAGGAGCAGACAAATATTTTGGTATCAATAATGACACATTTGCTGGATCTTCCCTCTTAC
 AAGCTAGAGAGCAAGCTGGTGTGCGGAAACTGCGAGCAGCACCAGGCTGGGAGGACTTTTGCAGGCGCCAGAT
 CATGCTGGGCTGTGAAGTCCAAAGTTGCCAGCTGATTTGTACAGACATCTGATGAGACTCTCTGCAACCCAGTT
 GCTGAGAGTACTTCTATCCGGCTGGCCCATGATTGCTTTCAGAAATGCCAACCACTCTTCTACTATGACGTGGGA
 CGCTGCCCTCTTAAGACTTTGTGAGGGCAGCAGGATAATGGATCAGTGCCTGGTGATGCTGCGAGACTGCTGTGT
 GGCATCTCCAGACAGGAGAAAGGAGATTCAGTGGCTGGTTCAGCTGCTCACCAAGGTGGCGAAGAGTGC
 AGCTGCGACGSGTGTACGGAAACTCGGAGCATCTGCGGGGCGCTGTGAGTGTGCTGACATGGGAGGCCCATG
 CGCTTTGGCCATCTGTACATGGGGAACAGCCGTGTAAGCATGACTGGCTACAAGGGCAGCTTTCACCTCCATGTC
 CCCAGGACATGAGAGAGCTGGTGTGCTCACATTTGTGGACAGGCTGCAGAAGTTTGTCAACACCACAAAGTGCTA
 CTTTTCACAAAGGAAGGGGAGTGGCGTGTTCATGAATCAAGATGCTTCTCGGAAAGAGGCCATCACTTTGGAA
 GCGATGGAGACCAACATCATCCCCGGGGGGAAGTGGTGGTGAAGACCATGGCTGAACGTGGAGATTTCCATCC
 AGGAGTTTCTACAGGCAGATGGGGAGCCCTACATAGGAAAGTGAAGGCGAGTGTGACCTTCTCGGATCCCCG
 AATATTTCCAGGCGACAGCTGSCCAGACTGACCTGAACCTTCATCAATGACGAAGAGAGACTTTCCCGCTCGG
 ACGTAGGATGCTCTCTGTCGATCTCAGAGATGAGTCTCAGAGCATTAATGTTGCAAAATGAGCTG
 CACTTGACTCGACCCAGGTCAAGATGCCAGNACATATCCAGAGTGAATCTGGTCACTCAATCCAGACACA
 GGGCTGTGGGAGGAGGAAGTGTATTTCAAATTTGAAATCAAAGGAGAACAAAGAGACAGAACTCTGCT
 GTGGGCAACTGGAGATTCGTGAGAGGAGGCTCTTTAACCCTGGATGTTCTTGAAGCAGGCGGTGCTTTTAAAG
 GTGAGGGCTACCCGGAGTGAAGGTTCTTGCTAGTGAGCAGATCCAGGGGGTGTGATGCTCCGTGATTAAGTC
 GAGCTTAGACTGGCTCTTGTGCCAACCTTAGGGCTCGGGGCGCTTTGACAGTGTATCATCAGAGGCCCAAGCGG
 GCGTGTGTCCTGCCCTCTGTGATGACCACTGCCCTGATGCCCTACTCTGCCATGTCTTGGCAAGCGCTGACTGGG
 GAGGAATCGCAGCTGAGGAGCTTCTTCTCAATTAACCCAAATGCAATTTGGCGTCCCTCAGCCCTATCTCAAC
 AAGCTCACTACCTGTGAGCGAGCATGAGGATCCAGGTTAAAGACAGCTTTCAGATTAGCATGSCAG
 CCAAGGCCCACTCAGCTGAGGAGACATGGGCCATCTATGCCCTTTGAGAAGCTCCGGGATGTGAAGAGGCA
 CCACCCAGTGCAGCCACTTCCGGTCTTACAGATTTAGGGGGATCGATATGACTACAACAGCTCCCCCTCAAC
 GAAGATGACCTATAGCTGGACTGAAGACTATCTGGCATGTTGGCCAAAGCGATGGAATTCAGGGGCTGCTAT
 ATCAAGGTGAAGATTTGTGGGCGCACTGGAAGTGAATGTGCGATCCCGCAACTGCGGGGGCATCTCATCGGGGACA
 GTGGGGAAGCTGTATGGAATCCGAGATGTGAGGAGCACTCGGACAGGACACAGCCCAATGTCTCAGCTGCCCTGT
 CTGGAGTTCAAGTGCAGTGGGATGCTCTATGCTCAGGAGCCGTGTGACCGCCAGCTTGGTGAAGGTCACTCCCGCAG
 GCGAGCTGCCCTGACGAGCTGTGAACCCATGCTGCTAGTACTGCTGGTCAACACTGCTGCACTGCACTGCACT
 AACGACACAGTGCAGCTGCTGCACTGCGACCTTGGAGCCAGCACTGCTGCACTGCACTGCACTGCACTGCACT
 GACCGAGCCCTCGCACGGCAGGAGATCGCGCTCGGGCGGTGCTTTGATGGCATCCGATGGCTCTTCCCA
 ATCATGAAGAGCAATTTGGGAGTGAAGCTTCACTTCACTGTGAGAGGAGCAATGAGCGCGAGAGTGGCTTC
 CAGTACTCCAAAGCAGCCAGCCAGCTCCCCGCTGCTCAGGACACTGTCCAAAGAGAGTSCCTCTGAGGAGGCGAG
 CAGCGAGCGTGAAGGGGTGGCCAGCCAGGCTGGATGGTGGCTCTCTGAGATTTCTAGAGTTGCTTGCATCTCAAC
 CCCCCTGATCAACTAAATTTTGTGATCTCACCTCTTCTGCGCTCAATTTGCTGTGACAGCCATTTGAGAGCTGA
 TGCACAAACTCACTTGGTATTTAATTTAAGCACTCTGTTTTCGTGAATTTGCTGTGTTTCTGTTCTGCGCTT
 CTTACTTTGTCCTGCTACTGATTTGGCAGCTGGGCCCAACAAATGGCACAATAAGGCCCTTTTGAATCTGTC
 TTTAAATGAACACAGATTTGGCACTGTAATCACTGCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 GCAATATATCTCTCTCTTTTGGCATGGTTTGGCCACTTGCATAGTATATCTGATGCTGAAGATCAA
 ATAAACCAATATAAGCATATTTTGGCTTGTCCACAGGACATAGGCAAGCTTGATCATAGTTTATACATAT
 AATGTGGTGAATAAAGAAATTAACACATATCTTTTACTTGAATTAATAACTATTTATTTTCTGCTA
 AATTTGGAATCTGCTGATCAATCAAAAGTTAAGTATTAATATAGGAGTATGATCATAGTTCTTCCAGAGTCTGG
 AAGAAGACTCTCTGATTTCCACAAATACACAGGTTGCTAAGTATTTGTACATTTCCCTTGCATCTGCTGT
 GTTCTTGTCTAGAAACCAAGTGTAGCCAGGGCAGATGCAATAAATGCTACTCTGATATTTGCAAAAAA

412/550

FIGURE 412

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPGEWTTWFNID
YPGGKG DYERLDAIRFYYGDRVCARPLRLEARTDWTTPAGSTQGVVHGSPEGFWCLNREQRP
GQNCNSYTVRFLCPPGSLRRDTERIWSFWSFWSKCSAACGQTGVQTRTRICLAEMVSLCSEAS
EEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGA VSLPGGAPASGAAYLLTKTPKL
LTQTDSDGRFRIPGLCPDGK SILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPYMVMNP
ETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAGEYFCKA
QSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQ NATNSFYVDVGRCPVKTCAGQQ
DNGIRCRDAVQNC CGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRVSAADNGEP
MRFGHVYMGNSRVSM TGYKGTFTLHVPQDTERLVITFVDRLQKFVNTTKVLPFNKKGSAVFHE
IKMLRRKEPITLEAMETNI IPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKVKASVTFDPR
NISTATAAQTDLNF INDEGDTFPLRTYGMFSVD FRDEVTSEPLNAGKVKVHLDSTQVKMPEHI
STVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNLDPESRRCFVKV
RAYRSE RFLPSEQIGGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGACVPAFCDDQSPDA
YSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLN YRRTDHEDPRVKKTAFAQISM AKPR
PNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDNTVPFNEDDPMSWTE DYLAWW
PKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRSTRDRDQPNVSAACLEF
KCSGMLYDQDRVDRTL VKVIPQGSRRASVNPLMHEYLVNHLPLAVNNDTSEYTMLAPLDPLG
HNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNV GVALTFNCVERQVGRQSAFQYLQ
STPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFP RVAQQPLIN

413/550

FIGURE 413

GCCACGTTGTCTTCTTTCTTCACCACCACCCAGGAGCTCAGAGATCTAAGCTGCTTTCCATC
TTTTCTCCCAGCCCCAGGACACTGACTCTGTACAGGAATGGGGCCGTCCTCTTGCCCTCCTTCTC
ATCCTAATCCCCCTTCTCCAGCTGATCAACCCGGGGAGTACTCAGTGTTCCCTAGACTCCGTT
ATGGATAAGAAGATCAAGGATGTTCTCAACAGTCTAGAGTACAGTCCCTCTCCTATAAGCAAG
AAGCTCTCGTGTGCTAGTGTCAAAGCCAAGGCAGACCGTCCTCCTGCCCTGCTGGGATGGCT
GTCCTGGCTGTGCTTGTGGCTATGGCTGTGGTTCGTGGGATGTTTCAGCTGGAAACCACTGC
CACTGCCAGTGCAGTGTGGTGGACTGGACCACTGCCCGCTGCTGCCACCTGACCTGACCAGGGGA
GGAGGCTGAGAACTCAGTTTTGTGACCATGACAGTAATGAAACCAGGGTCCCAACCAAGAAAT
CTAACTCAAACGTCCCACTTCATTTGTTCCATTCTGATTCTTGGGTAATAAAGACAAACTTT
GTACCTCAAAAAAAAAAAAAAAAAAAAAA

414/550

FIGURE 414

MGPSSCLLLILIPLLQLINPGSTQCSLDSVMDKKIKDVLNSLEYSPSPISKKLSCASVKS
QGRPSSCPAGMAVTGCACGYGCGSWDVQLETTCHCQCSVVDWTTARCCHLT

415/550

FIGURE 415

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGTG
AGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGCGGAGGAGGGCTGTGAGGA
GTGTGTGGAACAGGACC CGGGACAGAGGAACCATGGGCTCCGACGAACCTGAGCACCTTTTGCC
TGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTGGGGG
TGCCCTCGAAGTGCCCTCTATAAAGGATATTA AAAAGGCCCTATAGGAACTAGCCCTGCAGCTTC
ATCCCGACCGGAACCCCTGATGATCCACAAGCCCAGGAGAAATCCAGGATCTGGGTGCTGCTT
ATGAGGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAAGGATTAA
AAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTTTGGTTTCA
TGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATATTATTGTAG
ATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTTAGAAACAAAC
CTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGATGCGGACCACCC
AGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAATGCCCTAATGTCA
AACTAGTGAATGAAGAACGAACGCTGGAAAGTAGAAATAGAGCCTGGGGTGAGAGACGGCATGG
AGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCC
GAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATTTGTACACAAATGTGA
CAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACA
AGGTACATATTTCCCGGATAAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAG
GGCTCCCCA ACTTTGACAACAACAATATCAAGGGCTCTTTGATAATCACTTTTGATGTGGATT
TTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAACAGCTACTGAAACAAGGGT
CAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGAATAAAATTTGACTTTGT
AAAAAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTGTGTGTGTTTTGTTTTTA
TTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGATCATCATGAAATGAATAAGAGG
GCTTAAGAATTTGTCCATTTGCATTTCGAAAAGAAATGACCAGCAAAAGGTTTACTAATACCTC
TCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGTTTCAAGAATTAAAGCTGCAAGAGG
ACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGTTGTTAGCAATTTCAATCAAATG
CCA ACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTTTA

416/550

FIGURE 416

MAFQNLSTFCLLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHFD RNPDDPQAQEKFDLGAAYE
VLSDSEKRKQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQDRNIPRGSDI IVDLEVTLEEVYAGNF
VEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQMTQEVV CDECPNVKLVNEERTLEVEIEPGVRDGM EYFFI
GEGEPHV DGE PGDLRFRIKVVKHPIFERRGDDLYTNVTISL VESLVGFEMDITHLDGHKVHISRDKITRPGA KLV
KKGEGLPNFDNNNIKGLIITFDVDFPKEQLTEEAREG I KQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

417/550

FIGURE 417

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTCCCAGCAGGA
TGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCGCCGGGCGAG
GATGACCAAGGCCCGGCTGTTCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCTGCT
GATCATCGTGTACTGGGACAGCGCAGGCGCGCGCACTTCTACTTGACACGTCCTTCTCTAG
GCCGCACACGGGGCCGCCCTGCCACGCCCGGGCCGGACAGGACAGGGAGCTCACGGCCGA
CTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGACCTTCC
CAGAAAGGAGACGGAGCAGCCGCCCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAGGCTACGA
CTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAGCGGAGGAG
CGTGCTSCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCGCGCATTTCGA
CGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGGCCATCTACTG
CTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTGAGCGGAAGCCT
GCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCACGTGCACAAACGC
CAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCGCTACGGGAAGCTCTCCCGCCACCTCAT
GAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCTGTCGCGGACCCCTTCGTGCGCCTGAT
CTCCGCCCTTCGCGAGCAAGTTTCGAGCTGGAGAACGAGGAGTTCTACCGCAAGTTCGCGCTGCC
CATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCTCGGCGCGCAGGGCCTTCGCGCG
TGGCCTCAAGGTGTCTTTCGCCAACTTCATCCAGTACCTGCTGGACCCGCACACGGAGAAGCT
GGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCACCCGTGCCAGATCGACTA
CGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGCAGCTGCTGCAGCTACTCCA
GGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGGACCGCCAGCAGCTGGGAGGA
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TGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCCATTGAGTACTGTATCGATATTGTT
TTTTAAGATTAATATATTTTCAGGTATTTAATACGA